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2002 (c) Action Potential
File 149:TGG Health&Wellness DB(SM) 1976-2003/Jun W1
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File 444:New England Journal of Med. 1985-2003/Jun W2
(c) 2003 Mass. Med. Soc.
File 467:ExtraMED(tm) 2000/Dec

Set Items Description
S1 23 NUCLEOLAR (S) RNA (S) TAR
S2 13 RD (unique items)
>>>KWIC option is not available in file(s): 399

2/3,K/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

14021055 BIOSIS NO.: 200300015084
A nucleolar TAR decoy inhibitor of HIV-1 replication.
AUTHOR: Michienzi Alessandro; Li Shirley; Zaia John A; Rossi John J(a)
AUTHOR ADDRESS: (a)Divisions of Molecular Biology, Beckman Research Institute of the City of Hope, 1450 East Duarte Road, Duarte, CA, 91010-3011, USA**USA E-Mail: jrossi@bricoh.edu
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 99 (22):p14047-14052 October 29 2002 2002
MEDIUM: print
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

...ABSTRACT: critical regulatory factor in HIV-1 gene expression. It mediates the transactivation of transcription from the HIV-1 LTR by binding to the transactivation response (*TAR*) element in a complex with cyclin T1. Because of its critical and early role in HIV gene expression, Tat and its interaction with the *TAR* element constitute important therapeutic targets for the treatment of HIV-1 infection. Based on the known *nucleolar* localization properties of Tat, we constructed a chimeric small *nucleolar* *RNA*-*TAR* decoy that localizes to the nucleoli of human cells and colocalizes in the nucleolus with a Tat-enhanced GFP fusion protein. When the chimeric *RNA* was stably expressed in human T lymphoblastoid CEM cells it potently inhibited HIV-1 replication. These results demonstrate that the *nucleolar* trafficking of Tat is critical for HIV-1 replication and suggests a role for the nucleolus in HIV-1 viral replication.

2/3,K/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07779643 BIOSIS NO.: 000092083014
HETEROLOGOUS BASIC DOMAIN SUBSTITUTIONS IN THE HIV-1 TAT PROTEIN REVEAL AN ARGININE-RICH MOTIF REQUIRED FOR TRANSACTIVATION
AUTHOR: SUBRAMANIAN T; GOVINDARAJAN R; CHINNADURAI G
AUTHOR ADDRESS: INST. MOL. VIROL., ST. LOUIS UNIV. MED. CENT., 3681 PARK AVE., ST. LOUIS, MO. 63110, USA.
JOURNAL: EMBO (EUR MOL BIOL ORGAN) J 10 (8). 1991. 2311-2318. 1991
FULL JOURNAL NAME: EMBO (European Molecular Biology Organization) Journal
CODEN: EMJOD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

...ABSTRACT: Tat protein coded by HIV-1 is a unique eukaryotic transactivator. It activates gene expression from the viral LTR by its interaction with a nascent *RNA* element (*TAR*) located at the 5 end of all HIV-1 transcripts. Tat appears to bind to its target *RNA* structure in a highly sequence-specific manner. The *TAR*-binding activity of Tat has been localized in an Arg-rich basic domain located between residues 49 and 57 of the Tat protein. We have carried out domain substitution studies with heterologous basic domains which are also implicated in *RNA* binding. Here, we report that a 19 or a 12 amino acid region from the N-terminus of HTLV-I Rex can functionally substitute for...

...to the nucleus and nucleolus. The chimeric Tat proteins containing the basic domains of Rex and the N proteins are also localized in the nuclear/*nucleolar* region. Since the functionally inative Tat - N chimeric proteins are still efficiently targeted to the nuclear/*nucleolar* compartments, our results suggest that nuclear/*nucleolar* localization alone is not sufficient for transactivation and demonstrate a direct role for the Arg motif in Tat function other than that required for nuclear/*nucleolar* localization.

2/3,K/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07320762 BIOSIS NO.: 000090100662
A BULGE STRUCTURE IN HIV-1 TAR RNA IS REQUIRED FOR TAT BINDING AND TAT-MEDIATED TRANS-ACTIVATION
AUTHOR: ROY S; DELLING U; CHEN C-H; ROSEN C A; SONENBERG N
AUTHOR ADDRESS: DEP. BIOCHEM., MCGILL UNIV., MONTREAL, QUEBEC, H3G 1Y6, CANADA.
JOURNAL: GENES DEV 4 (8). 1990. 1365-1373. 1990
FULL JOURNAL NAME: Genes & Development
CODEN: GEDEE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

...ABSTRACT: immunodeficiency virus type 1 (HIV-1) trans-activates viral gene expression and is obligatory for virus replication. Tat function is mediated through a sequence termed *TAR* that comprises part of the 5'-noncoding region of all HIV-1 mRNAs. This region forms a stable stem-loop structure in vitro. Recent evidence indicates that Tat binds directly to the *TAR* *RNA* sequence, and this binding is independent of the nucleotide sequence in the loop but dependent on the integrity of the upper stem. We used the...
...structure specificity of this interaction and its correlation with Tat trans-activation. We show that a 3-nucleotide bulge structure (positions +23 to +25) in *TAR* *RNA* is important for both Tat interaction with *TAR* *RNA* and Tat-mediated trans-activation of gene expression. Single base substitutions at position +23 that impair Tat-mediated trans-activation in vivo also reduce binding of Tat to *TAR* in vitro, suggesting that the first uridine residue in the bulge is the critical base for both functions. In contrast, mutations in the loop (positions...

...reduce Tat-mediated trans-activation, had no effect on Tat binding. We also show that a Tat peptide that includes the basic region required for *nucleolar* localization binds to *TAR* *RNA* with the same specificity as the full-length protein. We conclude that Tat binding to *TAR* is necessary but not sufficient by itself to account for trans-activation.

2/3,K/4 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

07360640 Genuine Article#: 155QX No. References: 81
Title: The yeast Saccharomyces cerevisiae YDL112w ORF encodes the putative 2'-O-ribose methyltransferase catalyzing the formation of Gm18 in tRNAs
Author(s): Cavaille J; Chetouani F; Bachellerie JP (REPRINT)
Corporate Source: UNIV TOULOUSE 3,CNRS, LBME, 118 ROUTE NARBONNE/F-31062 TOULOUSE//FRANCE/ (REPRINT); UNIV TOULOUSE 3,CNRS, LBME/F-31062 TOULOUSE//FRANCE/
Journal: RNA-A PUBLICATION OF THE RNA SOCIETY, 1999, V5, N1 (JAN), P66-81
ISSN: 1355-8382 Publication date: 19990100
Publisher: CAMBRIDGE UNIV PRESS, 40 WEST 20TH STREET, NEW YORK, NY 10011-4211
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

...Identifiers--SMALL *NUCLEOLAR* RNAS; ADENOSYLMETHIONINE-DEPENDENT METHYLTRANSFERASES; TRANSACTIVATING REGION *RNA*; HIV-1 *TAR* *RNA*; RIBOSOMAL-*RNA*; ESCHERICHIA-COLI; SEQUENCE MOTIFS; MESSENGER-*RNA*; SUBNUCLEAR LOCALIZATION; PSEUDOURIDINE SYNTHASE

2/3,K/5 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04255630 H.W. WILSON RECORD NUMBER: BGSA00005630 (USE FORMAT 7 FOR FULLTEXT)
Lentivirus replication and regulation.
AUGMENTED TITLE: review
Tang, Hengli
Kuhen, Kelli L; Wong-Staal, Flossie
Annual Review of Genetics v. 33 (1999) p. 133-70
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 17942

(USE FORMAT 7 FOR FULLTEXT)

TEXT:
... protein possesses the activation domain. Residues 48 through 57 comprise an arg/lys-rich basic region that is responsible both for direct interaction with the *TAR* *RNA* target and for nuclear/*nucleolar* localization. The arginine at aa position 52 is critical for this specific association with *TAR*. The carboxy-terminal region, encoded by exon 2, is dispensable for function.

At the transcriptional level, the Tat/TAR interaction can potentially enhance or stabilize...

2/3,K/6 (Item 1 from file: 266)
DIALOG(R)File 266:FEDRIP

00299035
IDENTIFYING NO.: 5R01AI50492-02 AGENCY CODE: CRISP
Modeling RNA-based HIV gene therapeutics in SCID-hu mice
PRINCIPAL INVESTIGATOR: AKKINA, RAMESH K
ADDRESS: AKKINA@LAMARCOLOSTATE.EDU COLORADO STATE UNIVERSITY COLLEGE OF BETERINARY MED & BIOL FORT COLLINS, CO 80523
PERFORMING ORG.: COLORADO STATE UNIVERSITY, FORT COLLINS, COLORADO
SPONSORING ORG.: NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES
DATES: 2001/01/02 TO 2012/31/06 FY : 2003

...SUMMARY: vector transduced hematopoietic progenitor cells. Several new exciting developments occurred recently in the areas of stem cell biology, lentiviral gene transfer vectors, ribozyme targeting, and *RNA*-based therapeutics and, therefore, the stage is currently set to achieve success. In the present proposal, we would like to exploit these new technologies and...

... Project 2) are interactive and complimentary to the objectives of accompanying interactive R01 proposal (Project 1) by J. Rossi entitled "Combinatorial use of anti-HIV *RNA* -based therapeutics." The specific objectives of our proposal are: 1) Determine the effect of retrovirally transduced pol III promoter driven *nucleolar* , nuclear and cytoplasmtargeted anti-HIV nbozymes *TAR* and RBE decoys, either individually or in combination, on the lineage specific differentiation of CD34+ cells into macrophages in vitro and into thymocytes in vivo in the SCID-hu thy/liv grafts and investigate the mechanism of action of *RNA* -based therapeutics in differentiated cells. 2) Determine the in vivo

protective effects of different anti-HIV-1 RNAs, individually and in combination, in SCID-hu...

2/3,K/7 (Item 2 from file: 266)
DIALOG(R)File 266:FEDRIP

00296693
IDENTIFYING NO.: 5R01AI42552-06 AGENCY CODE: CRISP
Combinatorial use of anti-HIV RNA-based therapeutics
PRINCIPAL INVESTIGATOR: ROSSI, JOHN J.
ADDRESS: JROSSI@COH.ORG BECKMAN RES INST OF CITY OF HOPE 1450 EAST DUARTE ROAD DUARTE, CA 91010-3011
PERFORMING ORG.: BECKMAN RESEARCH INST OF CITY OF HOPE, DUARTE, CALIFORNIA
SPONSORING ORG.: NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES
DATES: 2001/01/98 TO 2012/31/06 FY : 2003

...SUMMARY: transcriptase and protease for the treatment of HIV-1 infection. Patients on HAART have witnessed rapid decreases in blood and tissue levels of HIV-1 *RNA* and overall positive outcomes. Despite the overall success of HAART, reservoirs of HIV-1 continue to replicate in patients on HAART, necessitating prolonged and perhaps...

... overall goal of this program is to genetically modify human cells for resistance to HIV-1 infection and replication. To this end a series of *RNA* based anti-HIV-1 agents have been developed and tested. These inhibitory RNAs target multiple steps in the viral life cycle as well as the...

...led to the development of Pol III expressed, chimeric RNAs that localize the inhibitory RNAs to the cytoplasm, nucleus or nucleolus. We have shown that *nucleolar* localization of an anti-HIV-1 ribozyme, *TAR* or RBE decoy provides potent inhibition of viral replication. By combining the composition and intracellular localization of this collection of antiviral RNAs, it should be possible to achieve long-term, synergistic inhibition of HIV-1 replication. Importantly, the use of combinatorial inhibitory *RNA* therapy in conjunction with HAART may provide additional synergy, allowing reduced dosing of HAART reagents. The overall objectives of this proposal are to test the...

... inhibitory RNAs and several HAART reagents. This program is part of an interactive R01 program (Project 1) with Dr. Ramesh Akkina (Project 2) entitled "Modeling *RNA*-based HIV gene therapeutics in the SCID-hu mouse." The Specific Aims of this proposal are: 1) construction of retroviral and lentiviral vectors harboring multiple...

... RNAs and HAART agents in blocking infectious spread of HIV-1 in cell culture; 5) transduction of primary CD34+ cells with the single and combinatorial *RNA* expressing vectors to monitor differentiation in culture and differentiation in the SCID-hu mouse model. This aim is to be carried out collaboratively with Dr...

2/3,K/8 (Item 3 from file: 266)
DIALOG(R)File 266:FEDRIP

00295463
IDENTIFYING NO.: 2R37AI29329-14 AGENCY CODE: CRISP
Enhancing the Intracellular Functioning of HIV Ribozymes
PRINCIPAL INVESTIGATOR: ROSSI, JOHN J
ADDRESS: JROSSI@COH.ORG BECKMAN RES INST OF CITY OF HOPE 1450 EAST DUARTE ROAD DUARTE, CA 91010-3011
PERFORMING ORG.: BECKMAN RESEARCH INST OF CITY OF HOPE, DUARTE, CALIFORNIA

SPONSORING ORG.: NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES
DATES: 2007/03/96 TO 2006/30/07 FY : 2002

...SUMMARY: in and demonstrations of efficacy both in vitro and in vivo have taken place. Ribozymes have the attributes of site-specific cleavage of the target *RNA*, the potential for turning over multiple substrates, and general lack of toxicity since they do not encode proteins In order to attain the goal of using anti-HIV ribozymes for treatment of HIV infection, we have been exploring several important areas of ribozyme function. These include identifying optimal *RNA* target sites for ribozyme interaction, co-localization of ribozyme and HIV RNAs and optimizing ribozyme expression from the backbones of lentiviral and retroviral vectors. The...
... analyses of engraftment potential. This latter work will be carried out collaboratively with Dr. Bruce Torbett at the Scripps Research Institute. 2) Functional analysis of *nucleolar* trafficking of HIV RNAs and regulatory proteins and in vivo selection for anti-HIV *nucleolar* localized ribozymes. A *nucleolar* localized anti-HIV-1 ribozyme as well as *nucleolar* localized *TAR* an RJ3E decoys have provided potent inhibition of HIV-1 infection in cultured cells. We will extend our analyses of these constructs to primary CD34+ cells and T-lymphocytes as part of specific aim 1. In aim 2 further analyses of the functional role of HIV-1 *RNA* trafficking through the nucleolus will be explored. Specifically, we will investigate the possibility that 2'0-methyl covalent backbone modifications in the R region of HN-1 *RNA* are guided by a cellular small *nucleolar* *RNA*. We will engineer a small *nucleolar* *RNA* to misdirect 2'0 methylations to specific sites of protein interaction in the HIV *TAR* and R13E elements. Finally, an in vivo SELEX scheme will be developec to select for new targets, both in HIV-1 and cellular RNAs using a randomized binding arm library of *nucleolar* localized ribozymes. The results of the work proposed in this aim should extend our knowledge of the functional role of HIV *RNA* and protein trafficking through the nucleolus, and provide new ribozymes and other inhibitory RNAs for inhibition of HIV-1 infection. The overall objective of this work is tc enhance our understanding of HIV *RNA* localization via the use of ribozymes, and to identify the best ribozyme-HIV target strategies for future use in human gene therapy.

2/3,K/9 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0295759 DBR Accession No.: 2002-17606
A nucleolar TAR decoy inhibitor of HIV-1 replication - vector-mediated gene transfer and expression in host cell and polymerase chain reaction for use in HIV virus-1 gene therapy
AUTHOR: MICHIENZI A; LI S; ZAIA JA; ROSSI JJ
CORPORATE AFFILIATE: City Hope Natl Med Ctr City Hope Natl Med Ctr
CORPORATE SOURCE: Rossi JJ, City Hope Natl Med Ctr, Beckman Res Inst, Div Mol Biol, 1450 E Duarte Rd, Duarte, CA 91010 USA
ISSN: 0027-8424 CODEN: 0027-8424; PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AME; (2002) 99, 22, 14047-14052
LANGUAGE: English

...ABSTRACT: critical regulatory factor in HIV-1 gene expression. It mediates the transactivation of transcription from the HIV-1 LTR by binding to the transactivation response (*TAR*) element in a complex with cyclin T1. Because of its critical and early role in HIV gene expression, Tat and its interaction with the *TAR* element constitute important therapeutic targets for the treatment of HIV-1 infection. Based on the known *nucleolar* localization properties of Tat, we constructed a chimeric small *nucleolar* *RNA*-*TAR* decoy thatlocalizes to the nucleoli of human cells and colocalizes in the nucleolus with a Tat-enhanced GFP fusion protein. When the chimeric *RNA* was stably expressed in human T lymphoblastoid CEM cells it potently inhibited HIV-1 replication. These results demonstrate that the *nucleolar* trafficking of Tat iscritical for HIV-1 replication and

suggests a role for the nucleolus in HIV-1 viral replication. (6 pages)

2/3,K/10 (Item 1 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01313399 SUPPLIER NUMBER: 11517856 (USE FORMAT 7 OR 9 FOR FULL TEXT)
The AIDS virus: what we know and what we can do about it.
Wong-Staal, Flossie
The Western Journal of Medicine, v155, n5, p481(7)
Nov,
1991
PUBLICATION FORMAT: Magazine/Journal ISSN: 0093-0415 LANGUAGE: English
RECORD TYPE: Fulltext; Abstract TARGET AUDIENCE: Professional
WORD COUNT: 4527 LINE COUNT: 00463

... mechanisms, tat and rev also have several parallel features. They are both small nucleoproteins that are found predominantly in the nucleolus. Both of them recognize *RNA* rather than DNA targets, a feature that distinguishes them from most other viral transactivators. The target for rev is called the rev response element, or RRE, and the target for tat is *TAR*. In both cases, the *RNA* targets are highly structured molecules, and the recognition of them by the viral transactivators is largely structural. The rev gene product binds to a specific "hammerhead" (stem-loop II) region of the RRE, and tat binds to three unpaired bases in the so-called bulge of *TAR*. That binding of these viral transactivators to their target RNAs is not sufficient for function and that cellular factors are also involved are evident because...

...may not be functional. For example, the domain for binding to RRE has been mapped on the Rev protein. This region also doubles as the *nucleolar* targeting domain. In addition, there is another critical domain in which mutations do not affect the capability of the protein to bind to RRE, and ...

...that this region is an activator domain that mediates interaction of the Rev protein with cellular factor(s). Essential functional domains including the regions for *RNA* binding

2/3,K/11 (Item 2 from file: 149)
DIALOG(R)File 149:TGG Health&Wellness DB(SM)

01311360 SUPPLIER NUMBER: 10873149 (USE FORMAT 7 OR 9 FOR FULL TEXT)
Arginine-mediated RNA recognition: the arginine fork.
Calnan, Barbara J.; Tidor, Bruce; Biancalana, Sara; Hudson, Derek; Frankel, Alan D.
Science, v252, n5009, p1167(5)
May 24,
1991
PUBLICATION FORMAT: Magazine/Journal ISSN: 0036-8075 LANGUAGE: English
RECORD TYPE: Fulltext TARGET AUDIENCE: Academic
WORD COUNT: 3418 LINE COUNT: 00325

... RNA interaction. This could explain why interaction of HIV Tat or Rev with RNA causes a change in RNA conformation upon binding [5, 19].

Other *RNA*-protein interactions will likely follow some of the principles outlined here. Arginine-rich motifs similar to the basic region of Tat are found in several *RNA*-binding proteins, including bacterial antiterminators, ribosomal proteins, and HIV Rev [3]. Other *RNA*-binding proteins may bring basic amino acids together through protein tertiary structure rather than primary sequence and may position specific arginines to interact with defined *RNA* structures. For example, the U1 A protein, which contains a ribonuclear protein (RNP) *RNA*-binding motif, has a highly defined structure with a cluster of basic amino acids at one end and

at least one arginine that is essential...

...recognition [20]. It is not yet known if this arginine makes a base-specific or structure-specific contact. For TFIIIA, the strongest interactions with 5S *RNA* are localized to junctions between stems and loops [21], similar to the stem-bulge junction in *TAR*; perhaps arginines participate in some of these interactions. Arginine has also been shown to bind to the guanosine binding site of a group I intron [22]; however, this interaction involves H-bonding to a guanine base in the *RNA* and is distinct from the arginine fork proposed here. Many *RNA*-binding proteins, including heterogeneous nuclear *RNA*-binding proteins and *nucleolar* proteins, contain clusters of methylated arginines, most commonly [N.sup.G],[N.sup.G]-dimethylarginine [23]. Because methylation would block H-bonding but would not alter the charge of the side chain, arginine methylation could provide a mechanism to regulate *RNA* binding between specific and nonspecific modes. While it is clear the *RNA* recognition will involve more than just arginine forks, it seems reasonable to suggest that arginine-mediated recognition of *RNA* structure may be an important part of many *RNA*-protein complexes.

REFERENCES AND NOTES

[1] M. A. Rould, J. J. Perone, D. Soll, T. A. Steitz, Science, 246, 1135 (1989).

[2] P. J. Romaniuk...

2/3,K/12 (Item 1 from file: 159)

01915587 PMID: 93686277

HIV-1 transactivator.

No affiliation given
Harvard AIDS Inst Ser 1991, 1 p43-310,
Document Type: MONOGRAPH
Languages: ENGLISH
Main Citation Owner: NOTNLM
Record type: Completed

...viral regulatory proteins tat and rev, are expressed, whereas, late in infection production switches to full-length, unspliced transcripts that act both as the virion *RNA* and the mRNA for the gag-pol polyprotein. HIV-1 transactivator is reviewed in the following chapters: *RNA* interactions of the tat and rev proteins of HIV-1; the role of the *TAR* region and tat protein in HIV-directed gene expression; *RNA*-protein interactions required for regulation of HIV gene expression; cellular factors involved in regulating HIV gene expression; biochemical characterization of REV-RRE interaction; analysis of...

... the rex protein of HTLV-1; tat-mediated trans-activation as a presplicing event requiring a functional HIV-1 TATAA element; analysis of the TAT/*TAR* interaction in Xenopus oocytes; transcriptional regulation of HIV; functional topography of lentivirus tat proteins defined by domain switching; *nucleolar* targeting singles of HIV; characterization of the specific interaction between TAT and *TAR* *RNA* ; and the exogenous trans-activation activity of HIV-1 tat.

2/3,K/13 (Item 1 from file: 444)

00108320

Mechanisms of Disease: The Molecular Biology Of Human Immunodeficiency Virus Type 1 Infection (Review Article)

Greene, Warner C.
The New England Journal of Medicine
Jan 31, 1991; 324 (5),pp 308-317
LINE COUNT: 00566 WORD COUNT: 07820

TEXT
...of the HIV-1 genes (Fig. 4). Analyses of one-step HIV-1 growth curves reveal that the initial population of genomic-length viral messenger *RNA* (mRNA) molecules reaches the cytoplasm exclusively as fully-spliced, 2-kilobase viral transcripts (Ref. 44). These viral mRNAs uniquely encode the various regulatory proteins of...

...segment (Ref. 49). The cysteine-rich domain probably mediates dimerization of this transactivator, (Ref. 50) whereas the positively charged distal segment is responsible for both *RNA* binding and nuclear-*nucleolar* localization (Ref. 51). Thus far, no clear function has been ascribed to the proline-rich domain. *Figure 4.-Stages in the Expression of the HIV...

...1 allows early synthesis of the products of the HIV-1 regulatory genes, including the HIV-1 Tat protein (middle panel). Tat, acting through the *TAR* (transactivation response) element, functions as a potent amplifier of viral-gene expression, leading to a high level of expression of all sequences linked to the...
?